Herd-level risk factors for *Salmonella enterica* subsp. *enterica* in U.S. market pigs

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Abstract

Midwest U.S. herds ($n = 63$) were studied to identify risk factors for harboring *Salmonella enterica* among slaughter-weight pigs. Samples collected on farms (feces) and at slaughter (distal colonic content, cecal content and ileocolic lymph nodes) were cultured using conventional means. Approximately 15 pigs were studied per herd, for a total of 3754 samples. The proportion of pigs positive in one or more samples was calculated for each herd. Herd characteristics were described by a combination of interview and written survey. Logistic regression was used to detect relationships between the detection of *Salmonella* and potential herd-level risk factors. The mean individual pig prevalence was 5% for feces, 4% for distal colonic content, 15% for ileocolic lymph nodes, and 17% for cecal contents. One or more *Salmonella* isolates were detected in at least one sample type in every herd. The five most common serovars were *S.* Agona, *S.* Derby, *S.* Schwarzengrund, *S.* Typhimurium and *S.* Senftenberg, with 25 additional serovars detected. *Salmonella* prevalence estimates were positively correlated among all samples except distal colonic content and ileocolic lymph nodes. Pigs with culture positive fecal samples were at increased odds of being detected positive for each of the slaughter-collected samples examined, namely distal colonic content (OR = 30.5), ileocolic lymph nodes (OR = 12.9) and cecal content (OR = 23.2). Herds with positive fecal sample(s) had increased odds of having positive cecal content (OR > 1.5), distal colonic content (OR = 15.3) and ileocolic

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lymph nodes (OR = 12.7). Pigs from herds with at least some bowl drinkers had eight-fold higher odds of testing *Salmonella* positive than did pigs from herds with only nipple drinkers. Pigs from herds with only dry feeders had five-fold higher odds of testing *Salmonella* positive when compared with pigs from herds with combinations of wet/dry style feeders. Interventions at these two points should be considered when designing growing pig facilities to reduce *Salmonella* shedding.

1. Introduction

Salmonella enterica has been commonly identified on U.S. pig farms, with 38.2% of farms testing positive in a 1995 survey of the major swine producing states in the U.S. (Anon., 1997). Increasing pressure by consumers, regulators and processors has encouraged the production sector to explore methods to reduce *Salmonella* shedding at the time of slaughter. Public health risks associated with *Salmonella* infections should be evaluated at each link in the food chain, including the farmer/producer, an approach advocated for or implemented by certain countries in the production of pork and other animal-based foods (Hald et al., 2005; Hopp et al., 1999).

Potential risk factors should be identified and quantified as a precursor to the development of programs and procedures to economically and reliably reduce *Salmonella* shedding. It is important that this information be available before *Salmonella* reduction plans are implemented at the farm level to enable producers to retain market access, make informed choices, enhance public health and avoid unnecessary costs.

Fedorka-Cray et al. (1994) have shown that naïve swine exposed to an infected population shedding $\leq 10^3$ colony forming units/gram of feces can become infected with, and shed *S.* Typhimurium within 48 h post-exposure. Wood et al. (1989) documented that *S.* Typhimurium infections persist in several tissues of swine, including the tonsils, mandibular and ileocolic lymph nodes, ceca, large intestine and ileum for at least 28 weeks following experimental challenge in some pigs. In this study, 12 of 13 palantine tonsils and 6 of 13 cecal content samples were *Salmonella* culture positive 16–28 weeks post-infection. Pigs among three naturally infected farms were estimated to shed for an average of 18–26 days, with a range up to 101 days (Kranker et al., 2003). Thus, it appears that pigs can potentially remain a risk to food safety for *Salmonella* long after they have been infected.

Risk factors have been examined in recent studies and a summary of recent literature shows that diverse risk factors have been identified (Funk and Gebreyes, 2004). In The Netherlands, reduced risk of *Salmonella* positive culture status has been associated with automated liquid feeding of by-products as well as membership of an Integrated Quality Control production group, while use of trough feeding was associated with an increased risk (van der Wolf et al., 1999). Nollet et al. (2004) demonstrated increased risk of culture positive mesenteric lymph nodes collected at slaughter for herds with a high proportion of solid flooring surfaces. Beloeil et al. (2004) reported increased risk of fecal shedding with concurrent *Lawsonia* or Porcine Reproductive and Respiratory Syndrome virus infection, infrequent removal of sow dung and failure to empty manure pits. Several studies have

reported factors associated with decreased *Salmonella* antibody detection in market swine, including feed and hygiene factors (Wong et al., 2004) and tylosin use (van der Wolf et al., 1999).

Thirty-two years ago, Edel et al. (1974) suggested it would be possible to produce pigs with a low prevalence of *Salmonella* infections if pigs were fed pelleted feeds, exposures to other animals, birds, people and insects were minimized, pigs were derived from *Salmonella*-free breeding stock, and strict biosecurity was maintained. Fedorka-Cray et al. (1997) showed that raising pigs free of *Salmonella* by use of isolated weaning techniques may be possible. However, *Salmonella* are still commonly isolated from apparently healthy pigs at or around the time of slaughter. For example, *Salmonella* were detected in 25 of 30 asymptomatic herds sampled at the time of slaughter (Bahnson et al., 2005).

Salmonella have been isolated from pigs both before and after shipment to slaughter, and consequently factors at both locations can provide risks of *Salmonella* contamination at the slaughter plant. *Salmonella* culture prevalence at slaughter has been correlated with farm collected samples at the herd level (Bahnson et al., 2005). Although not tested statistically, Kampelmacher et al. (1963) reported positive association between *Salmonella* culture results of fecal and distal colonic content samples at the individual level. Although the authors did not report an odds ratio of association in the 1963 paper, it can be calculated from the data reported as 12.3 when combining pigs with long and short transport times. To our knowledge the associations between *Salmonella* status of feces collected before shipment to slaughter and that of cecal content or ileocolic lymph nodes collected at slaughter have not been reported elsewhere. The herd-level associations suggest that it should be possible to make on-farm inferences from slaughter plant collected samples. However, transmission during transport to and lairage in the slaughter plant is possible (Swanenburg et al., 2001; Hurd et al., 2002; Rostagno et al., 2003). Samples collected at slaughter may contain *Salmonella* that originate on the farm, at the slaughter plant, or from trucks and intermediate holding facilities. Consequently, samples collected at slaughter provide a composite indication of on-farm, transit and in-plant risk factors.

This study was designed to describe the strength of association between potential herd-level risk factors and the detection of *Salmonella* in commercially produced, slaughter-weight pigs, and to describe the relationships between *Salmonella* bacterial culture results from pigs sampled before slaughter and again at the time of slaughter.

2. Materials and methods

2.1. Herd selection and data collection

Herds were eligible for this study if they were in the U.S. state of Minnesota and had voluntarily submitted pigs for veterinary herd health inspection at slaughter (Pointon et al., 1999) on one of the first 4 days of the week (Monday–Thursday) during the period May 1995 through April 1997. To reduce travel costs, herd selection was limited to those within a 200 km radius of the slaughter plant, which was one of the two large-scale slaughter plants in Minnesota. Eligible herds were contacted shortly before slaughter to obtain permission. A maximum of two herds were sampled per week. On weeks when more than

two herds were available for study, two were selected at random. Herds were eligible for inclusion in the study only once.

One of two technicians visited each herd 48 h or less prior to slaughter. With the herd manager or worker, the technician individually identified the animals to be shipped with a numbered ear tag and collected fecal samples. To ensure that at least 15 individuals were sampled both on the farm and at slaughter, 20 pigs were initially selected to allow for possible lost ear tags during shipment and slaughter. These individuals were a convenience sample of all those selected by the manager for shipment. Feces were collected from the non-disturbed surface of a fecal pat after observed defecation or by gentle digital extraction from the anus with a gloved hand. Gloves were changed between each animal.

A survey was administered by a combination of personal interview and written response. The survey was designed to collect information in the areas of health, facility design, hygiene and biosecurity, pig-flow management, transport and lairage. The field technician validated survey responses by direct visual inspection when possible. In cases where the survey could not be completed at the time of the visit, the incomplete survey was left with respondents and they were asked to return it by post. Of 68 farms sampled during the period, 63 returned surveys. Batch pig flow was defined as filling a room or barn over two weeks or less with pigs of similar age, with the condition that the room or barn was empty of pigs at the time of first entry for the current group. Good hygiene was defined as cleaning the facility with both high-pressure water and applying disinfectant prior to placement of pigs. Because these two variables were highly correlated, they were combined to form a single variable for analysis, GOOD HYGIENE-BATCH PIG FLOW.

2.2. Slaughter sample collection

Pigs were transported to slaughter using normal farm practices, held in lairage at the slaughter plant, and in some cases held at intermediate collection stations. Pigs in this study were held in pens separating them from other herds. In contrast, pigs from non-study herds were in some cases mixed with pigs from other herds if space restrictions so required. Although the lairage was periodically cleaned with scraping and cold water, disinfectants were not routinely applied between groups and consequently, fecal–oral contamination between study and non-study herds was possible.

After slaughter and evisceration, intestinal tracts were set aside for processing away from the production line. Distal colonic content and cecal content (10–20 g) were collected after opening the tracts with sanitized scalpel blades. Lymph nodes (>10 g) draining the cecum and ileum, referred to as ileocolic lymph nodes in the pig (Dyce et al., 2002), were collected after careful dissection and reflection of the overlying mesentery to prevent cross contamination between pigs. The surgical instruments used for dissections were sanitized in 82 °C water before each use. If the overlying mesentery was disrupted such that the lymph node tissue was exposed, the tract was discarded and another tract was substituted. Samples were packaged in individual sterile plastic bags, placed on ice within 2 h of collection, and sent to the laboratory on ice for processing the next day. While 20 pigs were tagged at the farm, only the first 15 carcasses on the processing line were sampled at the plant. All samples were matched at the level of the individual pig, while non-matching fecal samples collected only at the farm were discarded.

2.3. Laboratory procedures

All samples were qualitatively analyzed by conventional bacteriological methods designed for the isolation of *Salmonella* spp. (Fedorka-Cray et al., 1998) except that xylose lysine tergitol 4 agar was used (XLT4 Agar Base, Remel, Inc., Lenexa, Kansas) in conjunction with other plating media as described. Briefly, ∼1 g of feces or cecal contents was incubated in 10 ml tetrathionate broth (Tetrathionate Broth Base, Remel) and 10 ml GN Hajna broth (GN Broth, Remel) at 37 °C. Bagged lymph node samples were macerated by striking with a large mallet, and ∼5 g was incubated in 100 ml of each broth. Approximately 100 μl of GN Hajna broth were transferred into R-10 broth (Rappaport-Vassiliadis R-10 Broth, Remel) at 18–24 h, and an equal amount was transferred from tetrathionate broth to R-10 broth at 42–48 h. Both R-10 broths were incubated at 37 °C for 18–24 h. The broths were streaked for isolation on brilliant green agar with sulfadiazine (Brilliant Green Sulfa Agar, Remel) and XLT-4 agar, and the plates were incubated at 37 °C for 18–24 h. Colonies (1–3) exhibiting typical salmonellae-like morphology were transferred to triple sugar iron agar and lysine iron agar slants for biochemical confirmation. Confirmed isolates were serotyped at the National Veterinary Services Laboratory (U.S. Department of Agriculture, Animal Plant Health Inspection Service, Ames, Iowa, USA).

2.4. Data description and analysis

The prevalence of *Salmonella* was calculated for each of the samples collected. Spearman's correlation coefficients were calculated for the prevalence estimated for each of the four samples. At the individual pig level, odds ratios were calculated to assess the strength of association between *Salmonella* detection at the farm gate and the other three samples collected. Exact statistical methods were used to provide confidence intervals for associations (Cytel Software Corp., 1999). For further analysis, individuals were categorized *Salmonella* positive (SALPOS) if any of the four samples were *Salmonella* positive, and the proportion positive per herd calculated.

Responses to survey questions were used to produce variables for further analysis (Table 1). Survey analysis was limited to the last barn occupied prior to slaughter, that is, the "finisher" barn. To reduce the chance for spurious findings the total number of variables was limited to 14 main effects in the initial analysis, as indicated in Table 1 by variables with 51 valid responses.

Within-herd prevalence was estimated, accounting for the herd clusters, using SAS PROC SURVEYFREQ (SAS Institute, Inc., Cary, North Carolina, USA). Associations between *Salmonella* culture results and potential risk factors were assessed by logistic regression analysis. Herd was included as a random effect in logistic–normal regression models to account for the expected clustered nature of the dependent variable, SALPOS (Curtis et al., 1993) using Egret software version 2.0.1 (Cytel Software, Cambridge, Massachusetts, USA). Candidate variables were screened at the univariate level, and those with a Wald *p*-value of <0.25 were included in the starting model. Stepwise backward elimination was used with a *p*-value for retention of variables set to <0.05 for the Wald statistic, following procedures outlined by Hosmer and Lemeshow (2000). Interactions between variables were tested and retained if the *p*-value <0.05.

Table 1
Potential risk factors for *Salmonella* shedding in finisher pigs, assessed by an interview survey of 51 commercial U.S. pig producers during 1995–1997

Risk value and short description	Proportion or mean value	No. of herds[a]
Age at slaughter (days)	173.2	45
Growth promoting use of antibiotics	77.3%	44
Therapeutic use of antibiotics	40.9%	44
Animal source feed ingredients	52.1%	48
Birds access to pig area	21.6%	51
Some or all bowl drinkers	39.2%	51
Pigs delivered through an intermediate collection station	29.4%	51
Diagnosis of *Salmonella* infection in the past 12 months	13.7%	49
Feeders that do not allow mixing of feed and water	80.4%	51
Batch pig flow with good hygiene between batches[b]	53.9%	51
Diarrhea noted among in-contact pigs	11.8%	51
Domestic animal access to the pig area	25.5%	51
Pig access to outdoor pens	11.8%	51
Pen divisions open space allows pig to pig contact	90.2%	51
All flooring slotted or perforated	62.7%	51
Amount of space allocated per pig (m^2)	77.7%	37
Pigs selected for poor growth performance	21.6%	51
Time from leaving the farm until slaughter (h)	17 h 26 min	51
Transport vehicle was washed clean and sanitized	12.8%	47
Transport vehicle not owned by the farm	56.9%	51
Transport vehicle used on >1 herd during prior 30 days	50.0%	50

[a] Number of (valid) observations that contributed to the analysis presented.
[b] See the full text for description of batch pig flow and good hygiene.

As indicated in Table 1, eight additional variables were considered using a separate approach. Answers to these survey questions were missing for one or more herds for each of these variables. Consequently these models were made from slightly varying data sets, with decreased number of cases when these variables were added. Variables were retained if the Wald *p*-value was <0.05. To guard against the possibility of changing coefficients due to the differing cases (herds) included, the expanded models were reassessed for consistency with the base model.

Prevalence was estimated for those factors included in the final model by two methods. First, arithmetic means were calculated, breaking the herds down by their observed categories. Second, fitted odds were calculated from the model, and prevalence risk was estimated by the formula:

$$prevalence\_risk = \frac{odds}{1 + odds}$$

3. Results

The mean number of pigs per barn was 379 (S.D. 201), with a range of 110–1200. Pigs were reared from birth to market weight by 86% of the herds, with 14% of herds obtaining

growing pigs from other herds. In all herds, pigs were sequentially transferred to a least one different location (barn or room) after weaning; 43% of herds moved pigs to two and 41% moved pigs to three post-weaning locations. When moving to slaughter, the combined transport and lairage time averaged 17 h 26 min (S.D. 6 h 6 min) and ranged from 3 h 36 min to 32 h 24 min.

The minimum, maximum and average times of transport were 28 min, 5 h 2 min, and 1 h 26 min; the corresponding times for lairage were 2 h 52 min, 31 h 40 min and 15 h 21 min. Batch flow was practiced in finishers on 75% of farms; however, 22% of farms practiced batch flow but used inadequate sanitation, as defined above. The average number of samples processed per farm/sample type was slightly less than the target of 15 due to the occasional loss of samples in processing; the average sample sizes per herd were 14.8 for fecal samples, 14.9 for distal colonic content, and 15.0 for cecal and ileocolic lymph nodes.

A total of 419 *Salmonella* isolates were detected among 3754 samples processed (Table 2). The estimated within-herd prevalence was 27.9% (95% CI 20.5%, 35.3%), and ranged from 0 to 100% (Fig. 1). Twenty-seven distinct antigenic types were recognized. The five serovars most commonly isolated and the number of such isolates were *S.* Agona (110), *S.* Derby (72), *S.* Schwarzengrund (41), *S.* Typhimurium (48) and *S.* Senftenberg (30). These serovars accounted for 71.8% of all isolates.

At the herd-level, pair-wise comparisons of *Salmonella* prevalence between sample types were positively correlated for 5 of 6 pairs (Table 3). Herds with ≥1 positive fecal sample were at increased odds of having ≥1 positive of any of the slaughter-collected samples (Table 2). Individuals with a *Salmonella* positive farm fecal sample had increased odds of detection in each of the slaughter samples collected (Table 2).

Complete survey data for the 13 factors included in the initial model were available for 51 of the 63 herds. No difference was found when comparing *Salmonella* prevalence for herds with complete and incomplete survey responses (27.7% and 24.8%, respectively, $p = 0.74$).

Logistic regression (Table 4) produced models with two risk factors, namely feeder designs that did not provide for feed and water mixing and the use of some or all drinkers

Table 2

The prevalence of *S. enterica* detected and odds ratio associations at the individual- and herd-levels among samples collected from 63 U.S. swine herds at the farm (feces) and at slaughter (cecal content, distal colonic content, ileocolic lymph nodes) during 1995–1997

| Sample	Proportion *Salmonella* test-positive				Odds ratios of association with farm fecal culture result			
	Individual level			Herd level	Individual level		Herd level	
	%	95% CI	No. of pigs	%	OR	95% CI	OR	95% CI
Cecal content	17.4	11.1–23.7	942	63.5	23.2	10.0–60.2	+∞	1.50–+∞
Distal colonic content	3.9	1.4–6.5	937	22.2	30.5	13.4–69.9	15.3	2.6–106.7
Feces	4.9	0.9–9.0	934	15.9	n.a.	n.a.	n.a.	n.a.
Ileocolic lymph nodes	14.5	8.6–20.3	941	49.2	12.9	6.6–26.0	12.7	1.5–573.3
Any positive (SALPOS)	27.9	20.5–35.3	942	100	n.a.	n.a.	n.a.	n.a.

n.a.: not applicable.
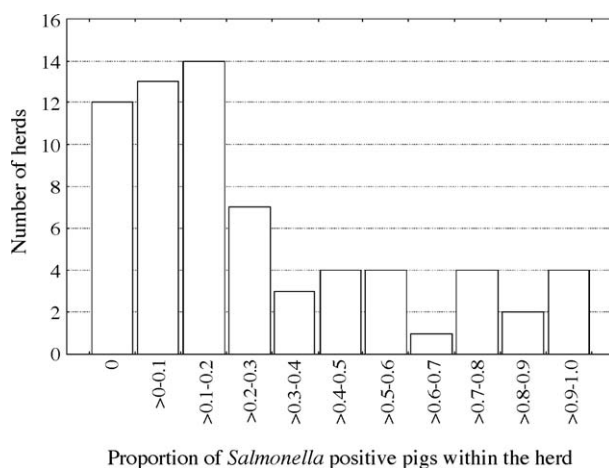
Fig. 1. The proportion of pigs with *Salmonella enterica* detected in one or more of four samples (feces, distal colonic content, cecal content, and ileocolic lymph nodes) collected near the time of slaughter from 51 U.S. swine herds during 1995–1997.

Table 3
Spearman's correlation coefficients (r) and associated p-values among *Salmonella* prevalence in four sample types collected from 63 U.S. swine herds during 1995–1997

Samples collected at slaughter	Collection point		
	Slaughter		Farm
	Ileocolic lymph nodes, r (p)	Cecal content, r (p)	Feces, r (p)
Distal colonic content	0.239 (0.06)	0.444 (<0.01)	0.579 (<0.01)
Ileocolic lymph nodes		0.281 (0.03)	0.498 (<0.01)
Cecal content			0.472 (<0.01)

Approximately 15 pigs were sampled from each herd.

Table 4
A logistic regression model linking herd characteristics to the odds of *Salmonella* culture positive test results among 764 pigs from 51 U.S. commercial swine herds sampled just prior to and at slaughter during 1995–1997

Category and terms	Coefficient	S.E.	p-Value[a]	Odds ratio	95% CI
Intercept	−3.73	0.698	<0.001		
Feed presentation					
Dry feed only	1.59	0.580	0.006	4.9	1.5–15.3
Combined wet/dry	0	n.a.	n.a.	1.0	n.a.
Drinker design					
Some or all bowl drinkers	2.08	0.523	<0.001	8.0	2.9–22.4
Nipple drinkers only	0	n.a.	n.a.	1.0	n.a.
Scale	1.89	0.327	n.a.	n.a.	n.a.

Deviance 140.6, 47 degrees of freedom. n.a.: not applicable or a reference category.
[a] This value was based on likelihood ratio chi-square.

Table 5
Prevalence[a] of *Salmonella* in 51 U.S. swine herds with or without two identified risk factors, contrasted with prevalence estimated by a logistic regression model

Type of feeding	Prevalence (%)			
	Observed		Estimated from the model	
	Nipple drinkers	Bowl drinkers	Nipple drinkers	Bowl drinkers
Wet/dry feed	4.4	24.8	2.3	16.1
Dry feed	21.0	49.2	10.6	48.7

Sampling was conducted during 1995–1997.

[a] Prevalence was estimated by combining the bacterial culture results of four samples (feces, distal colonic and cecal contents and ileocolic lymph nodes) for each of 15 pigs sampled from each herd.

with bowls to collect water. From the base model, forward stepwise model building did not identify additional factors for inclusion among the eight potential risk factors with missing survey responses. No statistical interactions were detected between the risk factors. Observed and fitted *Salmonella* prevalence were contrasted based on combinations of the risk factors identified (Table 5).

4. Discussion

The *Salmonella* fecal prevalence reported here, 4.9%, is comparable to the 6.0% positive samples reported in an U.S.D.A. study of 1447 representative herds from 17 of the top swine producing U.S. states. In contrast, the proportion of herds with one or more positive fecal samples was lower in this study, 15.6%, when compared with the U.S.D.A. study at 58.1% (Anon., 1997). Methodologies in the laboratory and field were similar in these two studies, including the culture of ~1 g fecal samples (Fedorka-Cray, P.J., unpublished data). However, the U.S.D.A. survey included herds from a broader geographic area and sampled more pigs per farm, differences that may explain the higher proportion of herds with one or more samples detected positive in the national survey. The fact that all herds sampled in this study had at least one *Salmonella* positive sample, coupled with the high proportion of both pigs and herds detected with *Salmonella* in cecal content and ileocolic lymph nodes suggests that intestinal content provides a substantial risk for contamination of pork carcasses thereby justifying care to avoid contamination during the slaughter process.

Drinker design was an important factor associated with risk of *Salmonella* carriage at the time of market. The nipple drinker design, associated with eight-fold lower odds when compared with bowl or bowl/nipple combination drinkers, is a design that would prevent water pooling where contamination with fecal material is possible, and consequently should reduce transmission among pen mates. In contrast, fecal or oral contamination of drinker bowls may increase the likelihood of transmission. Drinker design has not been reported a risk factor for *Salmonella* shedding or *Salmonella* antibodies in swine in prior published research, although drinker design has been associated with differing *Salmonella* isolation rates in turkeys (Renwick et al., 1992). One report from the Netherlands indicates that a trough combination drinker/feeder design was not associated with increased serologic prevalence (van der Wolf et al., 2001) while a related study found that same

practice to be associated with increased shedding (van der Wolf et al., 1999). Bowl drinkers can reduce water wastage and facilitate training newly weaned pigs to use the drinkers. However, when installing drinkers, farmers should consider that the nipple water design may offer protection against transmission of *Salmonella*. Further research on this topic is warranted, especially since the effect size detected was substantial, with an estimated prevalence difference attributable to waterer design of 14% among herds using wet/dry feeders, and 38% among herds with dry feeders (Table 5).

Providing feed in dry form was contrasted with feeder designs that provided for mixing of dry feed and water at the point of consumption, a design that can be referred to as "wet/dry." Wet/dry feeders were associated with lower risk of *Salmonella* shedding. These feeders allow for the feed to be mixed with water for a variable length of time, although not for the extended periods used in fermented feeding systems. Wet/dry feeders have been shown to reduce water disappearance, increase feed intake and improve feed efficiency in some trials when compared with dry feeders (Kim et al., 2000). The rationale for the apparent protective effect against *Salmonella* carriage is not clear based on currently available research, although the findings are consistent with studies associating other liquid feeding systems (Stege et al., 1999; van der Wolf et al., 1999; Wong, 2001) or liquid feed with fermented byproducts with decreased risk of detection of *Salmonella* antibodies (van der Wolf et al., 2001). In contrast, wet feeding in long common troughs has been associated with increased risk of culture positive status (van der Wolf et al., 1999). Taken together, the results of these studies suggest that additional research on the mechanism of effect of wet feed on *Salmonella* shedding is warranted, in part because of the relatively large difference in prevalence attributable to wet vs. dry feed presentation estimated from the current study, ranging from 8% to 33% for herds using nipple and bowl drinkers, respectively (Table 5).

This study failed to identify associations between any of the other potential risk factors considered and *Salmonella* detection. It is important to note, however, that a lack of detected association does not imply that the factor is biologically unrelated to *Salmonella* shedding. The relatively small number of herds studied, in conjunction with the fact that only herd-level risk factors were evaluated, suggests that the power to detect relationships, especially those of low to moderate effect size, is limited. Further, the culture of a 1 g sample for fecal and distal colonic content samples may have resulted in decreased sensitivity, resulting in a lower estimated prevalence, as has been reported by Funk et al. (2000) with a culture protocol using buffered peptone water pre-enrichment and comparing 1 and 10 g fecal samples. Observational studies, such as the current design, can detect relationships only for those potential risk factors with variation in the population. We were not able to analyze factors of biological interest because of lack of variation in the study population. In addition, other factors such as prior diagnosis of *Salmonella* were reported but not commonly, likely resulting in diminished power to detect relationships.

The farms included were a convenience sample of herds participating in a voluntary herd health data program at slaughter. Consequently, these farms may differ from those that did not participate in the program. The proportion of farms practicing batch pig flow in finishers was higher in the current study (75% versus 42%) as was the proportion of farms using veterinary service (100% versus 42%) when compared with the national U.S.D.A. study referenced above (Anon., 1995). However, pigs in the current study were of a similar age at slaughter as reported in the U.S.D.A. study (173 versus 176 days), had a similar

proportion of farms with farrowing included as a production phase (86% versus 71%) and a similar percentage were reared indoors-only during the finishing phase (68% versus 62%).

Salmonella prevalence for five of the six sample pairs were correlated, a finding similar to that reported by Sørensen et al. (2004), where positive correlations were found among samples collected from cecal content, cecal lymph nodes, carcass swabs and pharyngeal tonsils. Taken together, these studies suggest that results from one sample type might be used to approximate findings of another sample for certain epidemiologic studies and other applications where a high degree of precision is unnecessary. Correlation at the herd level does not imply that the test results at the individual level would be predictive, nor does it evaluate potential bias in test results at either the herd- or individual-level (Bland and Altman, 1986). However, the substantially higher herd- and individual-level odds of culture positive status at slaughter, given fecal culture positive status, suggests that culture results from farm collected fecal samples are predictive of slaughter results, and vice versa.

This importance of the herd as a primary source of slaughter plant *Salmonella* is further documented by the observation that pigs culture-positive at the farm were at substantially increased risk to test positive in subsequent samples. Further, finding nearly identical prevalence in fecal material collected on the farm and distal colonic content at the slaughter plant suggests that this sample, in particular, can be a useful proxy for on-farm collected fecal samples. Culture findings in fecal samples were an unbiased, though imprecise, predictor of culture results from distal colonic content. Although positively associated, fecal samples were a biased, imprecise predictor of both ileocolic lymph node and cecal content test results.

A moderate correlation between prevalence in farm- and slaughter plant-collected samples was also reported in a study of 30 herds marketed at a different Midwestern U.S. slaughter plant (Bahnson et al., 2005). The methods used were similar to the current study, except that in the 30-herd study more pigs were sampled (30) per herd, a larger fecal sample (10 g) was processed, and the only slaughter-collected sample was ileocolic lymph node tissue. These findings contrast with a study of five herds where weak associations were noted between on-farm and slaughter plant collected samples (Gebreyes et al., 2004) and a study of six herds demonstrating much higher prevalence of *Salmonella* detected in identical tissues collected from pen mates with or without transportation to slaughter (Hurd et al., 2002). The current study reports findings from a substantially larger number of herds, and thus might be expected to provide more robust results based on larger sample size. However, rapid infection and dissemination has been reported in an experiment that simulated heavy contamination during transportation and lairage (Hurd et al., 2001a); consequently, it is possible that in situations where heavy exposure to *Salmonella* occurs after pigs leave the farm, or where a high proportion of pigs are naive to *Salmonella*, a lower level of concordance might be expected.

Variation in transportation and lairage time was not a statistically significant risk factor, in spite of the fact that substantial variation in transport and lairage time was noted among these herds. These findings are consistent with that of Hurd et al. (2001b) and Nollet et al. (2004). A challenge study indicated that both feed withdrawal and transport to slaughter increased risk of test positive status when compared with pigs that were neither transported nor had their feed withdrawn prior to slaughter, while no increase risk of shedding was seen after transport among pigs that had been briefly feed deprived (Isaacson

et al., 1999). Hurd et al. (2002) demonstrated higher prevalence at slaughter after transport and lairage among herds liquidated during a disease eradication program. Taken together, these findings prompt us to speculate that while variation in transport and lairage time does not appear to be a critical factor, at least within the range observed in this study, the act of transportation itself, regardless of time, and/or the feed withdrawal associated with transport and lairage, may increase the risk of culture positive status. It should be noted, however, that herds with very long transport times were not eligible for the current study due to the 200 km maximum distance between herd and slaughter plant used as part of the herd selection criteria.

In conclusion, salmonellae were commonly detected in swine produced by commercial herds in Minnesota. Based on high prevalence detected in both cecal content and ileocolic lymph nodes, *Salmonella* should be regarded as an important risk to pork food safety, justifying measures to prevent contamination of pork at slaughter. Nipple drinkers were associated with decreased risk of *Salmonella* detection, and use of this drinker design should be considered to reduce the risk of transmission of *Salmonella* between pen-mates. The provision of feed mixed with water rather than providing feed in dry form only was also associated with decreased detection, and should be further investigated as a possible intervention point. Finally, based on the strong associations between farm and slaughter plant culture results, *Salmonella* infection at the farm appears to be an important source of *Salmonella* at slaughter. Consequently, farm-level interventions should be considered as part of comprehensive programs to reduce *Salmonella* contamination of pork.

Acknowledgments

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